

SEQUENCE LISTING

<110> Della Penna, Dean
Collakova, Eva
Coughlan, Sean J.
Helentjaris, Timothy G.

<120> PHYTYL/PRENYLTRANSFERASE NUCLEIC ACIDS,
POLYPEPTIDES AND USES THEREOF

<130> 1095R

<150> US 09/307,460

<151> 1999-05-07

<160> 29

<170> FastSEQ for Windows Version 3.0

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<211> 1616

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (108)...(1286)

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	Met Glu Ser
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ctg ctc tct agt tct tct ctt gtt tcc gct gct ggt ggg ttt tgt tgg	164
Leu Leu Ser Ser Ser Ser Leu Val Ser Ala Ala Gly Gly Phe Cys Trp	
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aag aag cag aat cta aag ctc cac tct tta tca gaa atc cga gtt ctg	212
Lys Lys Gln Asn Leu Lys Leu His Ser Leu Ser Glu Ile Arg Val Leu	
20 25 30 35	
cgt tgt gat tcg agt aaa gtt gtc gca aaa ccg aag ttt agg aac aat	260
Arg Cys Asp Ser Ser Lys Val Val Ala Lys Pro Lys Phe Arg Asn Asn	
40 45 50	
ctt gtt agg cct gat ggt caa gga tct tca ttg ttg ttg tat cca aaa	308
Leu Val Arg Pro Asp Gly Gln Gly Ser Ser Leu Leu Leu Tyr Pro Lys	
55 60 65	
cat aag tcg aga ttt cgg gtt aat gcc act gcg ggt cag cct gag gct	356
His Lys Ser Arg Phe Arg Val Asn Ala Thr Ala Gly Gln Pro Glu Ala	
70 75 80	
ttc gac tcg aat agc aaa cag aag tct ttt aga gac tcg tta gat gcg	404
Phe Asp Ser Asn Ser Lys Gln Lys Ser Phe Arg Asp Ser Leu Asp Ala	
85 90 95	
ttt tac agg ttt tct agg cct cat aca gtt att ggc aca gtg ctt agc	452

Phe Tyr Arg Phe Ser Arg Pro His Thr Val Ile Gly Thr Val Leu Ser	
100	105 110 115
att tta tct gta tct ttc tta gca gca gag aag gtt tct gat ata tct	500
Ile Leu Ser Val Ser Phe Leu Ala Ala Glu Lys Val Ser Asp Ile Ser	
120	125 130
cct tta ctt ttc act ggc atc ttg gag gct gtt gtt gca gct ctc atg	548
Pro Leu Leu Phe Thr Gly Ile Leu Glu Ala Val Val Ala Ala Leu Met	
135	140 145
atg aac att tac ata gtt ggg cta aat cag ttg tct gat gtt gaa ata	596
Met Asn Ile Tyr Ile Val Gly Leu Asn Gln Leu Ser Asp Val Glu Ile	
150	155 160
gat aag gtt aac aag ccc tat ctt cca ttg gca tca gga gaa tat tct	644
Asp Lys Val Asn Lys Pro Tyr Leu Pro Leu Ala Ser Gly Glu Tyr Ser	
165	170 175
gtt aac acc ggc att gca ata gta gct tcc ttc tcc atc atg agt ttc	692
Val Asn Thr Gly Ile Ala Ile Val Ala Ser Phe Ser Ile Met Ser Phe	
180	185 190 195
tgg ctt ggg tgg att gtt ggt tca tgg cca ttg ttc tgg gct ctt ttt	740
Trp Leu Gly Trp Ile Val Gly Ser Trp Pro Leu Phe Trp Ala Leu Phe	
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gtg agt ttc atg ctc ggt act gca tac tct atc aat ttg cca ctt tta	788
Val Ser Phe Met Leu Gly Thr Ala Tyr Ser Ile Asn Leu Pro Leu Leu	
215	220 225
cgg tgg aaa aga ttt gca ttg gtt gca gca atg tgt atc ctc gct gtc	836
Arg Trp Lys Arg Phe Ala Leu Val Ala Ala Met Cys Ile Leu Ala Val	
230	235 240
cga gct att att gtt caa atc gcc ttt tat cta cat att cag aca cat	884
Arg Ala Ile Ile Val Gln Ile Ala Phe Tyr Leu His Ile Gln Thr His	
245	250 255
gtg ttt gga aga cca atc ttg ttc act agg cct ctt att ttc gcc act	932
Val Phe Gly Arg Pro Ile Leu Phe Thr Arg Pro Leu Ile Phe Ala Thr	
260	265 270 275
gcg ttt atg agc ttt ttc tct gtc gtt att gca ttg ttt aag gat ata	980
Ala Phe Met Ser Phe Phe Ser Val Val Ile Ala Leu Phe Lys Asp Ile	
280	285 290
cct gat atc gaa ggg gat aag ata ttc gga atc cga tca ttc tct gta	1028
Pro Asp Ile Glu Gly Asp Lys Ile Phe Gly Ile Arg Ser Phe Ser Val	
295	300 305
act ctg ggt cag aaa cgg gtg ttt tgg aca tgt gtt aca cta ctt caa	1076
Thr Leu Gly Gln Lys Arg Val Phe Trp Thr Cys Val Thr Leu Leu Gln	
310	315 320
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Met Ala Tyr Ala Val Ala Ile Leu Val Gly Ala Thr Ser Pro Phe Ile	
325	330 335
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Trp Ser Lys Val Ile Ser Val Val Gly His Val Ile Leu Ala Thr Thr	
340	345 350 355

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Phe Ser Val Thr Leu Gly Gln Lys Arg Val Phe Trp Thr Cys Val Thr				
305		310		320
Leu Leu Gln Met Ala Tyr Ala Val Ala Ile Leu Val Gly Ala Thr Ser				
	325		330	335
Pro Phe Ile Trp Ser Lys Val Ile Ser Val Val Gly His Val Ile Leu				
	340		345	350
Ala Thr Thr Leu Trp Ala Arg Ala Lys Ser Val Asp Leu Ser Ser Lys				
	355		360	365
Thr Glu Ile Thr Ser Cys Tyr Met Phe Ile Trp Lys Leu Phe Tyr Ala				
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ccc gtg cgg ccc ggc gcg gcc cgc ccg cga gat cat ttt cta cca cca	101
Pro Val Arg Pro Gly Ala Ala Arg Pro Arg Asp His Phe Leu Pro Pro	
15 20 25	
tgt tgt tcc ata caa cga aat ggt gaa gga cga att tgc ttt tct agc	149
Cys Cys Ser Ile Gln Arg Asn Gly Glu Gly Arg Ile Cys Phe Ser Ser	
30 35 40	
caa agg acc caa ggt cct acc ttg cat cac cat cag aaa ttc ttc gaa	197
Gln Arg Thr Gln Gly Pro Thr Leu His His His Gln Lys Phe Phe Glu	
45 50 55	
tgg aaa tcc tcc tat tgt agg ata tca cat cgg tca tta aat act tct	245
Trp Lys Ser Ser Tyr Cys Arg Ile Ser His Arg Ser Leu Asn Thr Ser	
60 65 70 75	
gtt aat gct tcg ggg caa cag ctg cag tct gaa cct gaa aca cat gat	293
Val Asn Ala Ser Gly Gln Gln Leu Gln Ser Glu Pro Glu Thr His Asp	
80 85 90	
tct aca acc atc tgg agg gca ata tca tct tct cta gat gca ttt tac	341
Ser Thr Thr Ile Trp Arg Ala Ile Ser Ser Ser Leu Asp Ala Phe Tyr	
95 100 105	
aga ttt tcc cgg cca cat act gtc ata gga aca gca tta agc ata gtc	389
Arg Phe Ser Arg Pro His Thr Val Ile Gly Thr Ala Leu Ser Ile Val	
110 115 120	
tca gtt tcc ctt cta gct gtc cag agc ttg tct gat ata tca cct ttg	437
Ser Val Ser Leu Leu Ala Val Gln Ser Leu Ser Asp Ile Ser Pro Leu	

ttc tac atg ttc atc tgg aag ctg ttc tac gcg gag tac ctg ctc atc 1205
Phe Tyr Met Phe Ile Trp Lys Leu Phe Tyr Ala Glu Tyr Leu Leu Ile
380 385 390 395

cct ctg gtg cgg tgagcgcgag gcgaggtggt ggcagacgga tcggcgtcgg 1257
Pro Leu Val Arg

cggggcggca aacaactcca cgggagaact tgagtgccgg aagtaaactc ccgtttgaaa 1317
gttgaagcgt gcaccaccgg caccgggcag agagagacac ggtggctgga tggatacggg 1377
tggccccccc aataaattcc cccgtgcatg gtacccacg ctgcttgatg atatcccatg 1437
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<212> PRT
<213> Zea mays

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35 40 45
Pro Thr Leu His His His Gln Lys Phe Phe Glu Trp Lys Ser Ser Tyr
50 55 60
Cys Arg Ile Ser His Arg Ser Leu Asn Thr Ser Val Asn Ala Ser Gly
65 70 75 80
Gln Gln Leu Gln Ser Glu Pro Glu Thr His Asp Ser Thr Thr Ile Trp
85 90 95
Arg Ala Ile Ser Ser Ser Leu Asp Ala Phe Tyr Arg Phe Ser Arg Pro
100 105 110
His Thr Val Ile Gly Thr Ala Leu Ser Ile Val Ser Val Ser Leu Leu
115 120 125
Ala Val Gln Ser Leu Ser Asp Ile Ser Pro Leu Phe Leu Thr Gly Leu
130 135 140
Leu Glu Ala Val Val Ala Ala Leu Phe Met Asn Ile Tyr Ile Val Gly
145 150 155 160
Leu Asn Gln Leu Phe Asp Ile Glu Ile Asp Lys Val Asn Lys Pro Thr
165 170 175
Leu Pro Leu Ala Ser Gly Glu Tyr Thr Leu Ala Thr Gly Val Ala Ile
180 185 190
Val Ser Val Phe Ala Ala Met Ser Phe Gly Leu Gly Trp Ala Val Gly
195 200 205
Ser Gln Pro Leu Phe Trp Ala Leu Phe Ile Ser Phe Val Leu Gly Thr
210 215 220
Ala Tyr Ser Ile Asn Leu Pro Tyr Leu Arg Trp Lys Arg Phe Ala Val
225 230 235 240
Val Ala Ala Leu Cys Ile Leu Ala Val Arg Ala Val Ile Val Gln Leu
245 250 255
Ala Phe Phe Leu His Ile Gln Thr Phe Val Phe Arg Arg Pro Ala Val
260 265 270
Phe Ser Arg Pro Leu Leu Phe Ala Thr Gly Phe Met Thr Phe Phe Ser
275 280 285
Val Val Ile Ala Leu Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Arg
290 295 300
Ile Phe Gly Ile Arg Ser Phe Ser Val Arg Leu Gly Gln Lys Lys Val
305 310 315 320
Phe Trp Ile Cys Val Gly Leu Leu Glu Met Ala Tyr Ser Val Ala Ile
325 330 335

Leu Met Gly Ala Thr Ser Ser Cys Leu Trp Ser Lys Thr Ala Thr Ile
 340 345 350
 Ala Gly His Ser Ile Leu Ala Ala Ile Leu Trp Ser Cys Ala Arg Ser
 355 360 365
 Val Asp Leu Thr Ser Lys Ala Ala Ile Thr Ser Phe Tyr Met Phe Ile
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 385 390 395

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28

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32

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tta tta gcc tta ctc tgg tgg cgg agt cga gat gta cac tta gaa agc 816
Leu Leu Ala Leu Leu Trp Trp Arg Ser Arg Asp Val His Leu Glu Ser
260 265 270

aaa acc gaa att gct agt ttt tat cag ttt att tgg aag cta ttt ttc 864
Lys Thr Glu Ile Ala Ser Phe Tyr Gln Phe Ile Trp Lys Leu Phe Phe
275 280 285

tta gag tac ttg ctg tat ccc ttg gct ctg tgg tta cct aat ttt tct 912
Leu Glu Tyr Leu Leu Tyr Pro Leu Ala Leu Trp Leu Pro Asn Phe Ser
290 295 300

aat act att ttt tag 927
Asn Thr Ile Phe *
305

<210> 10
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<212> PRT
<213> Synechocystis

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Gly Asp Gly Asn Ser Val Asn Ser Pro Ala Ser Leu Asp Leu Val Phe
35 40 45
Gly Ala Trp Leu Ala Cys Leu Leu Gly Asn Val Tyr Ile Val Gly Leu
50 55 60
Asn Gln Leu Trp Asp Val Asp Ile Asp Arg Ile Asn Lys Pro Asn Leu
65 70 75 80
Pro Leu Ala Asn Gly Asp Phe Ser Ile Ala Gln Gly Arg Trp Ile Val
85 90 95
Gly Leu Cys Gly Val Ala Ser Leu Ala Ile Ala Trp Gly Leu Gly Leu
100 105 110
Trp Leu Gly Leu Thr Val Gly Ile Ser Leu Ile Ile Gly Thr Ala Tyr
115 120 125
Ser Val Pro Pro Val Arg Leu Lys Arg Phe Ser Leu Leu Ala Ala Leu
130 135 140
Cys Ile Leu Thr Val Arg Gly Ile Val Val Asn Leu Gly Leu Phe Leu
145 150 155 160
Phe Phe Arg Ile Gly Leu Gly Tyr Pro Pro Thr Leu Ile Thr Pro Ile
165 170 175
Trp Val Leu Thr Leu Phe Ile Leu Val Phe Thr Val Ala Ile Ala Ile
180 185 190
Phe Lys Asp Val Pro Asp Met Glu Gly Asp Arg Gln Phe Lys Ile Gln
195 200 205
Thr Leu Thr Leu Gln Ile Gly Lys Gln Asn Val Phe Arg Gly Thr Leu
210 215 220
Ile Leu Leu Thr Gly Cys Tyr Leu Ala Met Ala Ile Trp Gly Leu Trp
225 230 235 240
Ala Ala Met Pro Leu Asn Thr Ala Phe Leu Ile Val Ser His Leu Cys
245 250 255
Leu Leu Ala Leu Leu Trp Trp Arg Ser Arg Asp Val His Leu Glu Ser
260 265 270
Lys Thr Glu Ile Ala Ser Phe Tyr Gln Phe Ile Trp Lys Leu Phe Phe

Parameter	Estimate	Standard Error	t-Statistic	p-Value	95% Confidence Interval
Intercept	1.0000	0.0000	1.0000	1.0000	1.0000
Age	0.0000	0.0000	0.0000	1.0000	0.0000
Gender	0.0000	0.0000	0.0000	1.0000	0.0000
Education	0.0000	0.0000	0.0000	1.0000	0.0000
Income	0.0000	0.0000	0.0000	1.0000	0.0000
Health	0.0000	0.0000	0.0000	1.0000	0.0000
Marital Status	0.0000	0.0000	0.0000	1.0000	0.0000
Occupation	0.0000	0.0000	0.0000	1.0000	0.0000
Religion	0.0000	0.0000	0.0000	1.0000	0.0000
Political Affiliation	0.0000	0.0000	0.0000	1.0000	0.0000
Residence	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Frequency	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Duration	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Purpose	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Satisfaction	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Frequency (Interaction)	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Duration (Interaction)	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Purpose (Interaction)	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Satisfaction (Interaction)	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Frequency * Travel Duration	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Frequency * Travel Purpose	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Frequency * Travel Satisfaction	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Duration * Travel Purpose	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Duration * Travel Satisfaction	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Purpose * Travel Satisfaction	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Frequency * Travel Duration * Travel Purpose	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Frequency * Travel Duration * Travel Satisfaction	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Frequency * Travel Purpose * Travel Satisfaction	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Duration * Travel Purpose * Travel Satisfaction	0.0000	0.0000	0.0000	1.0000	0.0000
Travel Frequency * Travel Duration * Travel Purpose * Travel Satisfaction	0.0000	0.0000	0.0000	1.0000	0.0000

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11

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Val	Ile Val Ser Gly His Gly Leu Leu Ala Ser Thr Leu Trp Gln Arg				
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Ala	Gln Gln Phe Asp Ile Glu Asn Lys Asp Cys Ile Thr Gln Phe Tyr				
	225		230		235
Met	Phe Ile Trp Lys Leu Phe Tyr Ala Glu Tyr Phe Leu Ile Pro Phe				
		245		250	255
Val					

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 <213> Zea mays

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Ala Arg Phe Leu Ala Ala Pro Ala Ile Arg Val Ile Ser Pro Ser Arg	
20 25 30	
ccc gcg ctg ccg ctc ctc tca tcc gcc tcc gca ggc ggc ttc cct cac	144
Pro Ala Leu Pro Leu Leu Ser Ser Ala Ser Ala Gly Gly Phe Pro His	
35 40 45	
gcc tct cgc gct ccc tgc agt gcc gcc cgc gag cac cgc cgc ggc acc	192
Ala Ser Arg Ala Pro Cys Ser Ala Ala Arg Glu His Arg Arg Gly Thr	
50 55 60	
gtg cgg gaa tgc tct cga gct gat gct gct gga gca gct cca tta tca	240
Val Arg Glu Cys Ser Arg Ala Asp Ala Ala Gly Ala Ala Pro Leu Ser	
65 70 75 80	
aag aca ctg tta gac ctc aag gat tcc tgc tgg aga ttt tta agg cca	288
Lys Thr Leu Leu Asp Leu Lys Asp Ser Cys Trp Arg Phe Leu Arg Pro	
85 90 95	
cat aca atc cga gga act gct tta gga tcc ata gca ttg gtt gcg aga	336
His Thr Ile Arg Gly Thr Ala Leu Gly Ser Ile Ala Leu Val Ala Arg	
100 105 110	
gcc ttg ata gag aat tcc cat ctg ata aac tgg tgg ttg ata ttc aaa	384
Ala Leu Ile Glu Asn Ser His Leu Ile Asn Trp Trp Leu Ile Phe Lys	
115 120 125	
gca ttc tat gga ctt ggg gca ttg ata ttt ggc aat ggt tac ata gtt	432
Ala Phe Tyr Gly Leu Gly Ala Leu Ile Phe Gly Asn Gly Tyr Ile Val	
130 135 140	
ggg att aat cag atc tat gat gtt gct att gac aag gta aac aag cca	480
Gly Ile Asn Gln Ile Tyr Asp Val Ala Ile Asp Lys Val Asn Lys Pro	
145 150 155 160	
tat tta ccc att gct gct ggt gat ctc tca att cag tca gca tgg ttg	528
Tyr Leu Pro Ile Ala Ala Gly Asp Leu Ser Ile Gln Ser Ala Trp Leu	

	165		170		175	
ttg gtg ata tta ttt gca gct gca ggt ttt tca att gtt ata tca aac						576
Leu Val Ile Leu Phe Ala Ala Ala Gly Phe Ser Ile Val Ile Ser Asn						
	180		185		190	
ttt gga cct ttc att acc tct cta tac tgc ctt ggc cta ttt ctt ggc						624
Phe Gly Pro Phe Ile Thr Ser Leu Tyr Cys Leu Gly Leu Phe Leu Gly						
	195		200		205	
act ata tat tct gtt cct cca ttt aga ctg aag aga tat ccg gtt gct						672
Thr Ile Tyr Ser Val Pro Pro Phe Arg Leu Lys Arg Tyr Pro Val Ala						
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gct ttt ctt atc att gca acg gtt cgt ggt ttc ctt ctc aac ttt ggc						720
Ala Phe Leu Ile Ile Ala Thr Val Arg Gly Phe Leu Leu Asn Phe Gly						
	225		230		235	240
gtg tac tat gct act agg gct gca cta ggt ctt aca ttc caa tgg agc						768
Val Tyr Tyr Ala Thr Arg Ala Ala Leu Gly Leu Thr Phe Gln Trp Ser						
	245		250		255	
tcc cct gtt gct ttc att aca tgc ttc gtg aca cta ttt gct ttg gtc						816
Ser Pro Val Ala Phe Ile Thr Cys Phe Val Thr Leu Phe Ala Leu Val						
	260		265		270	
att gct ata acc aaa gat ctc cct gat gtt gaa gga gat cgc aag tat						864
Ile Ala Ile Thr Lys Asp Leu Pro Asp Val Glu Gly Asp Arg Lys Tyr						
	275		280		285	
caa ata tca act ttg gca aca aag ctt ggt gtc aga aat att gca ttc						912
Gln Ile Ser Thr Leu Ala Thr Lys Leu Gly Val Arg Asn Ile Ala Phe						
	290		295		300	
ctt gga tct ggt tta tta tta gca aac tat att gct gct att gct gta						960
Leu Gly Ser Gly Leu Leu Leu Ala Asn Tyr Ile Ala Ala Ile Ala Val						
	305		310		315	320
gct ttt acc atg cct cag gat ttc agg tgc act gta atg gtt cct gtg						1008
Ala Phe Thr Met Pro Gln Asp Phe Arg Cys Thr Val Met Val Pro Val						
	325		330		335	
cat gct gtc ctt gct ggt ggt tta att ttc cag aca tgg gtt ctg gag						1056
His Ala Val Leu Ala Gly Gly Leu Ile Phe Gln Thr Trp Val Leu Glu						
	340		345		350	
caa gcg aag tac aga aag gat gct att tcg cag tac tat cgg ttc ata						1104
Gln Ala Lys Tyr Arg Lys Asp Ala Ile Ser Gln Tyr Tyr Arg Phe Ile						
	355		360		365	
tgg aat ctc ttc tat gct gaa tat atc ttc ttc ccg tta ata tag						1149
Trp Asn Leu Phe Tyr Ala Glu Tyr Ile Phe Phe Pro Leu Ile *						
	370		375		380	
agagatcttg tagttcatct tgatcttggg ctacagccta attcatggga gcaaataaaa						1209
agagggagaa gttggcaaag tgaggtctgt tgtgcatatt ttcaacggaa acaatggagt						1269
agcaatattg ctatgctagg gttctgaagt tgtaggagct tttcgaagct tttacgatgt						1329
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gcttgagatc tgggtcccga cagatggcgg tggaacggcc aagacaagct tgtttcatgc						1509
cactcgaggt cgaggctaaa ccactacggc gtgctcttcc atgaaacgca gaaaactagg						1569
gaaatgacta tatatatggt gcaatacgtt gtatatatttc tgagtttcag ctcgatatata						1629

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 Pro Ala Leu Pro Leu Leu Ser Ser Ala Ser Ala Gly Gly Phe Pro His
 35 40 45
 Ala Ser Arg Ala Pro Cys Ser Ala Ala Arg Glu His Arg Arg Gly Thr
 50 55 60
 Val Arg Glu Cys Ser Arg Ala Asp Ala Ala Gly Ala Ala Pro Leu Ser
 65 70 75 80
 Lys Thr Leu Leu Asp Leu Lys Asp Ser Cys Trp Arg Phe Leu Arg Pro
 85 90 95
 His Thr Ile Arg Gly Thr Ala Leu Gly Ser Ile Ala Leu Val Ala Arg
 100 105 110
 Ala Leu Ile Glu Asn Ser His Leu Ile Asn Trp Trp Leu Ile Phe Lys
 115 120 125
 Ala Phe Tyr Gly Leu Gly Ala Leu Ile Phe Gly Asn Gly Tyr Ile Val
 130 135 140
 Gly Ile Asn Gln Ile Tyr Asp Val Ala Ile Asp Lys Val Asn Lys Pro
 145 150 155 160
 Tyr Leu Pro Ile Ala Ala Gly Asp Leu Ser Ile Gln Ser Ala Trp Leu
 165 170 175
 Leu Val Ile Leu Phe Ala Ala Ala Gly Phe Ser Ile Val Ile Ser Asn
 180 185 190
 Phe Gly Pro Phe Ile Thr Ser Leu Tyr Cys Leu Gly Leu Phe Leu Gly
 195 200 205
 Thr Ile Tyr Ser Val Pro Pro Phe Arg Leu Lys Arg Tyr Pro Val Ala
 210 215 220
 Ala Phe Leu Ile Ile Ala Thr Val Arg Gly Phe Leu Leu Asn Phe Gly
 225 230 235 240
 Val Tyr Tyr Ala Thr Arg Ala Ala Leu Gly Leu Thr Phe Gln Trp Ser
 245 250 255
 Ser Pro Val Ala Phe Ile Thr Cys Phe Val Thr Leu Phe Ala Leu Val
 260 265 270
 Ile Ala Ile Thr Lys Asp Leu Pro Asp Val Glu Gly Asp Arg Lys Tyr
 275 280 285
 Gln Ile Ser Thr Leu Ala Thr Lys Leu Gly Val Arg Asn Ile Ala Phe
 290 295 300
 Leu Gly Ser Gly Leu Leu Leu Ala Asn Tyr Ile Ala Ala Ile Ala Val
 305 310 315 320
 Ala Phe Thr Met Pro Gln Asp Phe Arg Cys Thr Val Met Val Pro Val
 325 330 335
 His Ala Val Leu Ala Gly Gly Leu Ile Phe Gln Thr Trp Val Leu Glu
 340 345 350
 Gln Ala Lys Tyr Arg Lys Asp Ala Ile Ser Gln Tyr Tyr Arg Phe Ile
 355 360 365
 Trp Asn Leu Phe Tyr Ala Glu Tyr Ile Phe Phe Pro Leu Ile
 370 375 380

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<213> Oryza sativa

<220>

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Met Asp Ser Leu Arg Leu Arg Pro Ser Leu Leu Ala Ala Arg Ala Pro	
1 5 10 15	
ggc gcg gcc tcg ctg ccg cct ctc cgg cga gat cac ttt cta cca cct	154
Gly Ala Ala Ser Leu Pro Pro Leu Arg Arg Asp His Phe Leu Pro Pro	
20 25 30	
tta tgt tct atc cat aga aat ggt aaa cgg cca gtt tct ttg tcc agc	202
Leu Cys Ser Ile His Arg Asn Gly Lys Arg Pro Val Ser Leu Ser Ser	
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caa agg acc caa ggt cct tcc ttc gat caa tgt cag aaa ttc ttt ggt	250
Gln Arg Thr Gln Gly Pro Ser Phe Asp Gln Cys Gln Lys Phe Phe Gly	
50 55 60	
tgg aaa tcc tcc cac cac agg ata cca cat cga cca aca tct agt tcc	298
Trp Lys Ser Ser His His Arg Ile Pro His Arg Pro Thr Ser Ser Ser	
65 70 75 80	
gct gac gct tcg gga caa cct cta caa tct tca gct gaa gca cat gat	346
Ala Asp Ala Ser Gly Gln Pro Leu Gln Ser Ser Ala Glu Ala His Asp	
85 90 95	
tca tca agt ata tgg aag cca ata tca tct tct ccg gat gca ttt tac	394
Ser Ser Ser Ile Trp Lys Pro Ile Ser Ser Ser Pro Asp Ala Phe Tyr	
100 105 110	
agg ttt tct cgg cca cat act gtc ata gga aca gca ctt agc ata gtc	442
Arg Phe Ser Arg Pro His Thr Val Ile Gly Thr Ala Leu Ser Ile Val	
115 120 125	
tca gtt tcg ctg cta gct gtt gag aat ttg tcc gat gtg tct ccc ttg	490
Ser Val Ser Leu Leu Ala Val Glu Asn Leu Ser Asp Val Ser Pro Leu	
130 135 140	
ttc ctc act ggt ttg ctg gag gca gtg gta gca gct ctt ttc atg aac	538
Phe Leu Thr Gly Leu Leu Glu Ala Val Val Ala Ala Leu Phe Met Asn	
145 150 155 160	
atc tat atc gtt gga ttg aat cag ttg ttc gac att gag ata gat aag	586
Ile Tyr Ile Val Gly Leu Asn Gln Leu Phe Asp Ile Glu Ile Asp Lys	
165 170 175	
gtt aac aag cca act ctt cca tta gca tct ggg gaa tat tct cct gca	634
Val Asn Lys Pro Thr Leu Pro Leu Ala Ser Gly Glu Tyr Ser Pro Ala	
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act gga gtt gca ctt gta tca gcc ttc gct gct atg agc ttt ggc ctt	682
Thr Gly Val Ala Leu Val Ser Ala Phe Ala Ala Met Ser Phe Gly Leu	
195 200 205	
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Gly Trp Ala Val Gly Ser Gln Pro Leu Phe Leu Ala Leu Phe Ile Ser	

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Leu	Cys	Ser	Ile	His	Arg	Asn	Gly	Lys	Arg	Pro	Val	Ser	Leu	Ser	Ser	
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Gln	Arg	Thr	Gln	Gly	Pro	Ser	Phe	Asp	Gln	Cys	Gln	Lys	Phe	Phe	Gly	
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Trp	Lys	Ser	Ser	His	His	Arg	Ile	Pro	His	Arg	Pro	Thr	Ser	Ser	Ser	
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Ala	Asp	Ala	Ser	Gly	Gln	Pro	Leu	Gln	Ser	Ser	Ala	Glu	Ala	His	Asp	
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Ser	Ser	Ser	Ile	Trp	Lys	Pro	Ile	Ser	Ser	Ser	Pro	Asp	Ala	Phe	Tyr	
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Arg	Phe	Ser	Arg	Pro	His	Thr	Val	Ile	Gly	Thr	Ala	Leu	Ser	Ile	Val	
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Ser	Val	Ser	Leu	Leu	Ala	Val	Glu	Asn	Leu	Ser	Asp	Val	Ser	Pro	Leu	
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Ile	Tyr	Ile	Val	Gly	Leu	Asn	Gln	Leu	Phe	Asp	Ile	Glu	Ile	Asp	Lys	
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Val	Asn	Lys	Pro	Thr	Leu	Pro	Leu	Ala	Ser	Gly	Glu	Tyr	Ser	Pro	Ala	
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Thr	Gly	Val	Ala	Leu	Val	Ser	Ala	Phe	Ala	Ala	Met	Ser	Phe	Gly	Leu	
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Gly	Trp	Ala	Val	Gly	Ser	Gln	Pro	Leu	Phe	Leu	Ala	Leu	Phe	Ile	Ser	
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Phe	Ile	Leu	Gly	Thr	Ala	Tyr	Ser	Ile	Asn	Leu	Pro	Phe	Leu	Arg	Trp	
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Lys	Arg	Ser	Ala	Val	Val	Ala	Ala	Leu	Cys	Ile	Leu	Ala	Val	Arg	Ala	
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Val	Ile	Val	Gln	Leu	Ala	Phe	Phe	Leu	His	Ile	Gln	Thr	Phe	Val	Phe	
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Arg	Arg	Pro	Ala	Val	Phe	Thr	Arg	Pro	Leu	Ile	Phe	Ala	Thr	Ala	Phe	
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Met	Thr	Phe	Phe	Ser	Val	Val	Ile	Ala	Leu	Phe	Lys	Asp	Ile	Pro	Asp	
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Ile	Glu	Gly	Asp	Arg	Ile	Phe	Gly	Ile	Lys	Ser	Phe	Ser	Val	Arg	Leu	
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Gly	Gln	Lys	Lys	Val	Phe	Trp	Ile	Cys	Val	Gly	Leu	Leu	Glu	Met	Ala	
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Gly	Thr	Ala	Leu	Gly	Ser	Ile	Ala	Leu	Val	Ala	Arg	Ala	Leu	Ile	Glu				
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Asn	Pro	Gln	Leu	Ile	Asn	Trp	Trp	Leu	Val	Phe	Lys	Ala	Phe	Tyr	Gly				
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Phe	Ala	Ala	Ala	Gly	Phe	Ser	Ile	Val	Val	Thr	Asn	Phe	Gly	Pro	Phe				
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Ile	Thr	Ser	Leu	Tyr	Cys	Leu	Gly	Leu	Phe	Leu	Gly	Thr	Ile	Tyr	Ser				
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Val	Pro	Pro	Phe	Arg	Leu	Lys	Arg	Tyr	Pro	Val	Ala	Ala	Phe	Leu	Ile				
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Ile	Ala	Thr	Val	Arg	Gly	Phe	Leu	Leu	Asn	Phe	Gly	Val	Tyr	Tyr	Ala				
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Thr	Arg	Ala	Ala	Leu	Gly	Leu	Thr	Phe	Gln	Trp	Ser	Ser	Pro	Val	Ala				
				245					250					255					
Phe	Ile	Thr	Cys	Phe	Val	Thr	Leu	Phe	Ala	Leu	Val	Ile	Ala	Ile	Thr				
			260					265					270						
Lys	Asp	Leu	Pro	Asp	Val	Glu	Gly	Asp	Arg	Lys	Tyr	Gln	Ile	Ser	Thr				
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Leu	Ala	Thr	Lys	Leu	Gly	Val	Arg	Asn	Ile	Ala	Phe	Leu	Gly	Ser	Gly				
	290					295					300								
Leu	Leu	Ile	Ala	Asn	Tyr	Val	Ala	Ala	Ile	Ala	Val	Ala	Phe	Leu	Met				
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Pro	Gln	Ala	Phe	Arg	Arg	Thr	Val	Met	Val	Pro	Val	His	Ala	Ala	Leu				
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Ala	Val	Gly	Ile	Ile	Phe	Gln	Thr	Trp	Val	Leu	Glu	Gln	Ala	Lys	Tyr				
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Thr	Lys	Asp	Ala	Ile	Ser	Gln	Tyr	Tyr	Arg	Phe	Ile	Trp	Asn	Leu	Phe				
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Pro Thr Ser His Arg Val Pro Ser Thr Ile Pro Thr Leu Asn Phe Ala
10 15 20

aaa cta tca ttc act aag gcc aca acg tcc caa cct ttg ttc tta gga
Lys Leu Ser Phe Thr Lys Ala Thr Thr Ser Gln Pro Leu Phe Leu Gly
25 30 35

95										100					105					
aga	cct	cac	aca	ggt	att	ggc	aca	gca	tta	agc	ata	att	tct	gtg	tcc		389			
Arg	Pro	His	Thr	Val	Ile	Gly	Thr	Ala	Leu	Ser	Ile	Ile	Ser	Val	Ser					
			110					115					120							
ctc	ctt	gct	ggt	gag	aaa	ata	tca	gat	ata	tct	cca	tta	ttt	ttt	act		437			
Leu	Leu	Ala	Val	Glu	Lys	Ile	Ser	Asp	Ile	Ser	Pro	Leu	Phe	Phe	Thr					
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ggt	gtg	ttg	gag	gct	gtg	ggt	gct	gcc	ctg	ttt	atg	aat	att	tat	att		485			
Gly	Val	Leu	Glu	Ala	Val	Val	Ala	Ala	Leu	Phe	Met	Asn	Ile	Tyr	Ile					
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ggt	ggt	ttg	aat	caa	ttg	tct	gat	ggt	gaa	ata	gac	aag	ata	aac	aag		533			
Val	Gly	Leu	Asn	Gln	Leu	Ser	Asp	Val	Glu	Ile	Asp	Lys	Ile	Asn	Lys					
155					160					165					170					
ccg	tat	ctt	cca	tta	gca	tct	ggg	gaa	tat	tcc	ttt	gaa	act	ggt	gtc		581			
Pro	Tyr	Leu	Pro	Leu	Ala	Ser	Gly	Glu	Tyr	Ser	Phe	Glu	Thr	Gly	Val					
			175					180						185						
act	att	ggt	gca	tct	ttt	tca	att	ctg	agt	ttt	tgg	ctt	ggc	tgg	ggt		629			
Thr	Ile	Val	Ala	Ser	Phe	Ser	Ile	Leu	Ser	Phe	Trp	Leu	Gly	Trp	Val					
		190						195					200							
gta	ggt	tca	tgg	cca	tta	ttt	tgg	gcc	ctt	ttt	gta	agc	ttt	gtg	cta		677			
Val	Gly	Ser	Trp	Pro	Leu	Phe	Trp	Ala	Leu	Phe	Val	Ser	Phe	Val	Leu					
		205					210					215								
gga	act	gct	tat	tca	atc	aat	gtg	cct	ctg	ttg	aga	tgg	aag	agg	ttt		725			
Gly	Thr	Ala	Tyr	Ser	Ile	Asn	Val	Pro	Leu	Leu	Arg	Trp	Lys	Arg	Phe					
	220					225					230									
gca	gtg	ctt	gca	gcg	atg	tgc	att	cta	gct	ggt	cgg	gca	gta	ata	ggt		773			
Ala	Val	Leu	Ala	Ala	Met	Cys	Ile	Leu	Ala	Val	Arg	Ala	Val	Ile	Val					
235					240					245					250					
caa	ctt	gca	ttt	ttc	ctt	cac	atc	cag	act	cat	gta	tac	aag	agg	cca		821			
Gln	Leu	Ala	Phe	Phe	Leu	His	Ile	Gln	Thr	His	Val	Tyr	Lys	Arg	Pro					
				255				260						265						
cct	gtc	ttt	tca	aga	tca	ttg	att	ttt	gct	act	gca	ttc	atg	agc	ttc		869			
Pro	Val	Phe	Ser	Arg	Ser	Leu	Ile	Phe	Ala	Thr	Ala	Phe	Met	Ser	Phe					
			270					275					280							
ttc	tct	gta	ggt	ata	gca	ctg	ttt	aag	gat	ata	cct	gac	att	gaa	gga		917			
Phe	Ser	Val	Val	Ile	Ala	Leu	Phe	Lys	Asp	Ile	Pro	Asp	Ile	Glu	Gly					
		285					290					295								
gat	aaa	gta	ttt																	

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 Thr Gly Leu Gly His Ala Val Leu Ala Ser Ile Leu Trp Phe His Ala
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aaa tct gta gat ttg aaa agc aaa gct tcg ata aca tcc ttc tat atg 1157
 Lys Ser Val Asp Leu Lys Ser Lys Ala Ser Ile Thr Ser Phe Tyr Met
 365 370 375

ttt att tgg aag cta ttt tat gca gaa tac tta ctc att cct ttt gtt 1205
 Phe Ile Trp Lys Leu Phe Tyr Ala Glu Tyr Leu Leu Ile Pro Phe Val
 380 385 390

aga tga ggatgcagcg gcaatattga cttgagaatt agttttgttt aaatggtgct 1261
 Arg *
 395

gcctttgtca caggccggct tggagtcgct acattagttt taagttttta attgctaatt 1321
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 35 40 45
 Leu Asn His His Tyr Lys Ser Ile Glu Gly Gly Cys Thr Cys Lys Lys
 50 55 60
 Cys Asn Ile Lys Phe Val Val Lys Ala Thr Ser Glu Lys Ser Phe Glu
 65 70 75 80
 Ser Glu Pro Gln Ala Phe Asp Pro Lys Ser Ile Leu Asp Ser Val Lys
 85 90 95
 Asn Ser Leu Asp Ala Phe Tyr Arg Phe Ser Arg Pro His Thr Val Ile
 100 105 110
 Gly Thr Ala Leu Ser Ile Ile Ser Val Ser Leu Leu Ala Val Glu Lys
 115 120 125
 Ile Ser Asp Ile Ser Pro Leu Phe Phe Thr Gly Val Leu Glu Ala Val
 130 135 140
 Val Ala Ala Leu Phe Met Asn Ile Tyr Ile Val Gly Leu Asn Gln Leu
 145 150 155 160
 Ser Asp Val Glu Ile Asp Lys Ile Asn Lys Pro Tyr Leu Pro Leu Ala
 165 170 175
 Ser Gly Glu Tyr Ser Phe Glu Thr Gly Val Thr Ile Val Ala Ser Phe
 180 185 190
 Ser Ile Leu Ser Phe Trp Leu Gly Trp Val Val Gly Ser Trp Pro Leu
 195 200 205
 Phe Trp Ala Leu Phe Val Ser Phe Val Leu Gly Thr Ala Tyr Ser Ile
 210 215 220
 Asn Val Pro Leu Leu Arg Trp Lys Arg Phe Ala Val Leu Ala Ala Met
 225 230 235 240
 Cys Ile Leu Ala Val Arg Ala Val Ile Val Gln Leu Ala Phe Phe Leu
 245 250 255
 His Ile Gln Thr His Val Tyr Lys Arg Pro Pro Val Phe Ser Arg Ser
 260 265 270
 Leu Ile Phe Ala Thr Ala Phe Met Ser Phe Phe Ser Val Val Ile Ala
 275 280 285
 Leu Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys Val Phe Gly Ile

290	295	300
Gln Ser Phe Ser Val Arg	Leu Gly Gln Lys Pro	Val Phe Trp Thr Cys
305	310	315
Val Ile Leu Leu Glu Ile	Ala Tyr Gly Val Ala	Leu Leu Val Gly Ala
325	330	335
Ala Ser Pro Cys Leu Trp	Ser Lys Ile Val Thr	Gly Leu Gly His Ala
340	345	350
Val Leu Ala Ser Ile Leu	Trp Phe His Ala Lys	Ser Val Asp Leu Lys
355	360	365
Ser Lys Ala Ser Ile Thr	Ser Phe Tyr Met Phe	Ile Trp Lys Leu Phe
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Tyr Ala Glu Tyr Leu Leu	Ile Pro Phe Val Arg	
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Met Asp Trp	
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ggg ctt gct ata tct tct cat cct aaa cct tat tca gtc aca act ggt	165
Gly Leu Ala Ile Ser Ser His Pro Lys Pro Tyr Ser Val Thr Thr Gly	
5 10 15	
gga aat ctc tgg cgg agt aaa cac acc acc aag aat att tac ttt gca	213
Gly Asn Leu Trp Arg Ser Lys His Thr Thr Lys Asn Ile Tyr Phe Ala	
20 25 30 35	
agt tct tgg ata tca aaa gct tca cga cac aaa agg gaa act caa ata	261
Ser Ser Trp Ile Ser Lys Ala Ser Arg His Lys Arg Glu Thr Gln Ile	
40 45 50	
gaa cat aat gtt ttg agg ttc caa caa cca agt ttg gat cat cat tac	309
Glu His Asn Val Leu Arg Phe Gln Gln Pro Ser Leu Asp His His Tyr	
55 60 65	
aaa tgc atc aga gga ggg tct aca tat caa gaa tgc aat aga aaa ttt	357
Lys Cys Ile Arg Gly Gly Ser Thr Tyr Gln Glu Cys Asn Arg Lys Phe	
70 75 80	
gtt gtg aag gca atc tct aaa caa cct ctt ggt ttt gaa gct cat gct	405
Val Val Lys Ala Ile Ser Lys Gln Pro Leu Gly Phe Glu Ala His Ala	
85 90 95	
tcc aat cct aag aac att ttg gac tct gtc aaa aat gta ttg tct gct	453
Ser Asn Pro Lys Asn Ile Leu Asp Ser Val Lys Asn Val Leu Ser Ala	
100 105 110 115	
ttc tac tgg ttt tcc tat cca tac aca atg att ggc ata aca tta tgc	501
Phe Tyr Trp Phe Ser Tyr Pro Tyr Thr Met Ile Gly Ile Thr Leu Cys	
120 125 130	
gca ttt tct tca tct ctt ctc gcg gtg gaa aaa tta tca gat ata tct	549

gga tct ttc tat atg ttc atc tgg aag cta ttg tat gca ggg ttc ttt 1317
 Gly Ser Phe Tyr Met Phe Ile Trp Lys Leu Leu Tyr Ala Gly Phe Phe
 390 395 400

ctc atg gca tta att aga tga ggatatcgtg gaaggcttaa acaatgttct 1368
 Leu Met Ala Leu Ile Arg *
 405

cgacacatac accaaaataa aaggaatata tgttttgcac ctaagattta ttaaataaag 1428
 ccgaatgttg gttcttgtat cattaagatt ttttttttaa ttgtcgaaga ctttatgtat 1488
 tcatattcac cttgacttct acggtcaa at ttttcataaa gtggaataaa agcaacttgg 1548
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 35 40 45
 Thr Gln Ile Glu His Asn Val Leu Arg Phe Gln Gln Pro Ser Leu Asp
 50 55 60
 His His Tyr Lys Cys Ile Arg Gly Gly Ser Thr Tyr Gln Glu Cys Asn
 65 70 75 80
 Arg Lys Phe Val Val Lys Ala Ile Ser Lys Gln Pro Leu Gly Phe Glu
 85 90 95
 Ala His Ala Ser Asn Pro Lys Asn Ile Leu Asp Ser Val Lys Asn Val
 100 105 110
 Leu Ser Ala Phe Tyr Trp Phe Ser Tyr Pro Tyr Thr Met Ile Gly Ile
 115 120 125
 Thr Leu Cys Ala Phe Ser Ser Ser Leu Leu Ala Val Glu Lys Leu Ser
 130 135 140
 Asp Ile Ser Leu Ser Phe Leu Ile Gly Val Leu Gln Gly Val Leu Pro
 145 150 155 160
 Gln Leu Phe Ile Glu Ile Tyr Leu Cys Gly Val Asn Gln Leu Tyr Asp
 165 170 175
 Leu Glu Ile Asp Lys Ile Asn Lys Pro His Leu Pro Met Ala Ser Gly
 180 185 190
 Gln Phe Ser Phe Lys Thr Gly Val Ile Ile Ser Ala Ala Phe Leu Ala
 195 200 205
 Leu Ser Phe Gly Phe Thr Trp Ile Thr Gly Ser Trp Pro Leu Ile Cys
 210 215 220
 Asn Leu Val Val Ile Ala Ser Ser Trp Thr Ala Tyr Ser Ile Asp Val
 225 230 235 240
 Pro Leu Leu Arg Trp Lys Arg Tyr Pro Phe Val Ala Ala Met Cys Met
 245 250 255
 Ile Ser Thr Trp Ala Leu Ala Leu Pro Ile Ser Tyr Phe His His Met
 260 265 270
 Gln Thr Val Val Leu Lys Arg Pro Ile Gly Phe Pro Arg Ser Leu Gly
 275 280 285
 Phe Leu Val Ala Phe Met Thr Phe Tyr Ser Leu Gly Leu Ala Leu Ser
 290 295 300
 Lys Asp Ile Pro Asp Val Glu Gly Asp Lys Glu His Gly Ile Asp Ser
 305 310 315 320
 Phe Ala Val Arg Leu Gly Gln Lys Arg Ala Phe Trp Ile Cys Val Ser
 325 330 335

Phe Phe Glu Met Ala Phe Gly Val Gly Ile Leu Ala Gly Ala Ser Cys
 340 345 350
 Ser His Phe Trp Thr Lys Ile Phe Thr Gly Met Gly Asn Ala Val Leu
 355 360 365
 Ala Ser Ile Leu Trp Tyr Gln Ala Lys Ser Val Asp Leu Ser Asp Lys
 370 375 380
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 Asp Ile Pro Asp Val Asp Gly Asp Arg Asp Phe Gly Ile Gln Ser Leu
 20 25 30
 agt gtg aga ttg ggg cca caa aga gtg tat cag ctc tgc ata agc ata 144
 Ser Val Arg Leu Gly Pro Gln Arg Val Tyr Gln Leu Cys Ile Ser Ile
 35 40 45
 ctg tta aca gcc tat ggg gct gcc act gta gta gga gct tca tcc aca 192
 Leu Leu Thr Ala Tyr Gly Ala Ala Thr Val Val Gly Ala Ser Ser Thr
 50 55 60
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 His Leu Leu Gln Lys Ile Ile Thr Val Ser Gly His Gly Leu Leu Ala
 65 70 75 80
 gtg aca ctt tgg cag aga gcg cgg cac ctt gag gtt gaa aac caa gcg 288
 Val Thr Leu Trp Gln Arg Ala Arg His Leu Glu Val Glu Asn Gln Ala
 85 90 95
 cgt gtc aca tca ttt tac atg ttc att tgg aag cta ttc tat gca aag 336
 Arg Val Thr Ser Phe Tyr Met Phe Ile Trp Lys Leu Phe Tyr Ala Lys
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 Leu Leu Thr Ala Tyr Gly Ala Ala Thr Val Val Gly Ala Ser Ser Thr
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 His Leu Leu Gln Lys Ile Ile Thr Val Ser Gly His Gly Leu Leu Ala
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 Val Thr Leu Trp Gln Arg Ala Arg His Leu Glu Val Glu Asn Gln Ala
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 His Ala Pro Thr Thr Ala Ala Arg Phe Leu Pro Ala Pro Ala Gly Arg
 15 20 25
 ggc agg cgc ccg tcg ccg ccg gcc gct tca cct atc ttc tcc tct gct 148
 Gly Arg Arg Pro Ser Pro Pro Ala Ala Ser Pro Ile Phe Ser Ser Ala
 30 35 40
 tcc acc cga ttc acc cag tcc ccg cgc gcc ccc tgc ggc gcc gcc cga 196
 Ser Thr Arg Phe Thr Gln Ser Pro Arg Ala Pro Cys Gly Ala Ala Arg
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 ccg cgc tgg cgc gac acc gtg cgg gca tgc tct caa gct ggt gca gct 244
 Pro Arg Trp Arg Asp Thr Val Arg Ala Cys Ser Gln Ala Gly Ala Ala
 60 65 70 75
 ggg cca gct cca ctg tca aag aca tta tca gac cta aag gat tcc tgc 292
 Gly Pro Ala Pro Leu Ser Lys Thr Leu Ser Asp Leu Lys Asp Ser Cys
 80 85 90
 tgg aga ttt tta agg cca cac aca att cgt gga act gct ttg gga tcc 340
 Trp Arg Phe Leu Arg Pro His Thr Ile Arg Gly Thr Ala Leu Gly Ser
 95 100 105
 aca gcc ttg gtt gct aga gca tta tta gag aat ccc caa ttg atc gat 388
 Thr Ala Leu Val Ala Arg Ala Leu Leu Glu Asn Pro Gln Leu Ile Asp
 110 115 120
 tgg cgc ttg gta ttc aaa gca tta tat ggc ctt gta gct ttg atc tgc 436
 Trp Arg Leu Val Phe Lys Ala Leu Tyr Gly Leu Val Ala Leu Ile Cys
 125 130 135
 ggc aac ggt tac att gtt ggg att aat cag atc tat gac att gga att 484

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agcaattttt	gtacatactg	tttgactggg	aggggaatag	agcggcgatg	cgacgaggat	1331
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